

REMARKS

Reconsideration is requested.

Claims 47 and 53-56 have been revised, without prejudice, to remove references hybridization and homology. Entry of the present Amendment is requested to, at a minimum, reduce the issues for appeal.

The indication that claim 46 contains allowable subject matter is acknowledged, with appreciation. See page 11 of the Office Action dated July 7, 2010.

Claims 1-4, 10, 12-17, 19-23, 29, 44-47, 49-51 and 53-56 are pending.

The Section 112, first paragraph "written description", rejection of claims 1-4, 10, 12-17, 19-23, 29, 44, 45, 47, 49-51 and 53-56 is traversed. The Section 112, first paragraph "enablement", rejection of claims 1-4, 10, 12-17, 19-23, 29, 44, 45, 47, 49-51 and 53-56 is traversed. Reconsideration and withdrawal of the rejections are requested in view of the evidence of record as well as the following comments.

The applicants again note that pages 14-15 of the Amendment After Final Rejection filed May 22, 2009 provided an alignment demonstrating the presence of the motifs in the homologues which were described in the application.

The Examiner's reference to the Federal Circuit decision of the University of California v. Eli Lilly and Co., on page 3 of the Office Action dated July 7, 2010 is noted. The applicants submit that a precise definition that defines the structural features of the claimed chemical genus that distinguishes it from other chemical structures has been presented in the present specification and is defined in the claims. The pending claims include precise structural features which clearly distinguish the claimed subject matter

from other structures, namely SEQ ID NO: 5, SEQ ID NO: 51, SEQ ID NO: 7, SEQ ID NO: 8 and SEQ ID NO: 9. A person of ordinary skill in the art will appreciate sequences that are encompassed by the claimed genus and which fall outside the claims. Moreover, one of ordinary skill in the art will appreciate that the applicants were in possession of the claimed invention at the time the application was filed.

Further, the specification describes a representative number of polynucleotide sequences that comprise the recited motifs and that encode a 2xC2H2 protein, that when overexpressed produced the desired result. The Declaration filed May 22, 2009, for example, provides results for the sequence of SEQ ID NOs 27, SEQ ID NO: 36 and SEQ ID NO: 28.¹ The specification demonstrates the effect with the sequence of SEQ ID NO: 1. Page 19 of the Amendment After Final Rejection filed May 22, 2009 provides an alignment of three (3) of the proteins encoded by the above SEQ ID NOs illustrating the presence of the claimed motifs in the protein sequences of SEQ ID NOs 2, 27 and 37.

The applicants have therefore provided four (4) examples of sequences that encode a 2xC2H2 protein that when overexpressed produced the desired result. One of ordinary skill in the art will appreciate that the applicants were in possession of the claimed invention at the time the application was filed.

¹ The applicants note that some of the SEQ ID NOs in the Declaration appear to have been switched, such as for example SEQ ID NO:27 is referred to as a nucleic acid sequence while it is in fact the amino acid sequence of the gene. Further, SEQ ID NOs 26, 28 and 36 are the nucleic acid sequences encoding the proteins with SEQ ID NOs 27, 29 and 37, respectively.

Furthermore, the specification contains ample written description to clearly show that the applicants were in possession of the claimed invention at the time of filing.

Consideration of the following in this regard is requested.

Zinc finger proteins comprising 2xC2H2 domains were known in the art at the time of filing. See for example page 2, lines 17 to 29 of the application. Sakamoto et al. (Gene 248 (1-2) 23-32 (2000) (of record)) is referred to on lines 18-20 of page 2 of the specification. In the "Introduction" of Sakamoto et al., it is stated that "The Cys₂/His₂-type zinc finger, also called the classical or TFIIIA-type finger, is one of the best-characterized DNA binding motifs found in eukaryotic transcription factors."

Sakamoto et al. further describe on page 25 column 2 other structural features common to two-fingered proteins. Sakamoto et al. described four genes: AZF1, AZF2, AZF3 and STZ encoding proteins of the two-fingered Cys₂ His₂-type. Sakamoto report that the four genes were placed on the same branch of a phylogenetic tree constructed based on the two zinc finger sequences, indicating their close structural and functional relationship. The article further reports the presence of three conserved regions, named B-box, L-Box, and DNL-box outside the zinc finger motifs, as in other members of the two-fingered Cys₂ His₂-type zinc finger protein family. The Sakamoto reference therefore clearly illustrates that zinc finger proteins comprising 2xC2H2 domains and their conserved motifs were known in the art at the time of filing, as was the close structural and functional relationship of such proteins.

Even though two-fingered zinc finger proteins were well known in the art at the time of filing, the specification provides ample written description of the conserved

motifs found in the sequences useful in the methods of the claimed invention. One of ordinary skill in the art will be able to identify sequences comprising the motifs of the claims, such as by the process described on pages 10 and 11 of the application. The C2H2 zinc finger motif is described on page 11 of the application as filed. The different conserved motifs are described on pages 12 to 14.

In view of our above comments as well as the evidence of record, the applicants submit that the claims are supported by an adequate written description.

The applicants further submit that one of ordinary skill in the art will be able to make and use the claimed invention, without requiring undue experimentation.

As note above, the applicants have provided four (4) examples of sequences falling within the current claims, and which produce the desired effect when expressed in a plant. Further, as described by Sakamoto et al., zinc finger proteins comprising 2xC2H2 domains and their conserved motifs were known in the art at the time of filing, as was the close structural and functional relationship of such proteins.

Methods for identifying other sequences falling within the claimed definitions would be routine for a person of ordinary skill in the art. Methods for the search and identification of sequences comprising the motifs of the claims are also described on, for example, pages 10 and 11 of the application as filed. The C2H2 zinc finger motif is described, for example, on page 11 of the application. The different conserved motifs are described on, for example, pages 12 to 14 of the specification. Methods for the transformation of plants with such sequences would also be routine in the art, as would be the evaluation of plants to determine whether the transgenic plants exhibit the

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claimed effects. There would be no undue experimentation required to identify and to determine whether other sequences falling within the claimed range also exhibit the claimed effects. From the teachings of Sakamoto and from the evidence provided in the record, other zinc finger proteins comprising 2xC2H2 domains and the claimed conserved motifs would also lead to the effects defined in the claims.

The claims are supported by an enabling disclosure.

Withdrawal of the Section 112, first paragraph, rejections is requested.

The claims are submitted to be in condition for allowance and a Notice to that effect is requested. The Examiner is requested to contact the undersigned, preferably by telephone, in the event anything further is required in this regard.

Respectfully submitted,

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